

seq ID NO: 1

Database : GenEmbl:*

- 1: gb_env:*
- 2: gb_pat:*
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- 7: gb_sts:*
- 8: gb_sy:*
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- 10: gb_vi:*
- 11: gb_ov:*
- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
	1	1134	100.0	1134	2	AX615029	AX615029	AX615029 Sequence	
	2	1134	100.0	3104	2	AX615036	AX615036	AX615036 Sequence	
	3	1134	100.0	3104	15	SPU45308	SPU45308	U45308 Synechococc	
	4	1134	100.0	110000	15	CP000100_05	CP000100_05	Continuation (6 of	
c	5	1134	100.0	110000	15	AP008231_10	AP008231_10	Continuation (11 o	
c	6	503.6	44.4	110000	15	BA000039_04	BA000039_04	Continuation (5 of	
	7	485.6	42.8	110000	15	BA000022_23	BA000022_23	Continuation (24 o	
c	8	485	42.8	110000	15	CP000239_10	CP000239_10	Continuation (11 o	
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Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
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SUMMARIES

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		Query Match	Length			
1	485.6	42.8	1230	7	US-10-369-493-26469	Sequence 26469, A
2	466.2	41.1	1107	7	US-10-369-493-43685	Sequence 43685, A
3	161.4	14.2	1785	8	US-10-437-963-75871	Sequence 75871, A
4	161.4	14.2	2065	8	US-10-424-599-18773	Sequence 18773, A
5	147.4	13.0	1879	8	US-10-424-599-18772	Sequence 18772, A
6	140.6	12.4	1716	8	US-10-767-701-8981	Sequence 8981, Ap
7	133.4	11.8	1949	8	US-10-425-114-30648	Sequence 30648, A
8	133.4	11.8	2077	9	US-10-425-115-47612	Sequence 47612, A
9	133.2	11.7	1295	9	US-10-425-115-52894	Sequence 52894, A

Database : Published_Applications_NA_New:*

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- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	163	14.4	2093	8	US-11-216-545-1059	Sequence 1059, Ap
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3	161.4	14.2	1633	6	US-10-449-902-2362	Sequence 2362, Ap
c 4	150.4	13.3	1950	7	US-11-218-305-5034	Sequence 5034, Ap
5	146	12.9	1908	8	US-11-216-545-1060	Sequence 1060, Ap
6	142.4	12.6	2131	6	US-10-449-902-15521	Sequence 15521, A
7	133.4	11.8	2850	7	US-11-218-305-18858	Sequence 18858, A
c 8	125.2	11.0	1314	7	US-11-218-305-24484	Sequence 24484, A
c 9	124.6	11.0	1927	7	US-11-218-305-24482	Sequence 24482, A
10	123	10.8	2031	6	US-10-449-902-7919	Sequence 7919, Ap
11	122.8	10.8	1294	6	US-10-449-902-3517	Sequence 3517, Ap
c 12	121.4	10.7	1666	7	US-11-218-305-24483	Sequence 24483, A
c 13	121	10.7	1921	7	US-11-218-305-24481	Sequence 24481, A
c 14	80	7.1	775	8	US-11-266-748A-80959	Sequence 80959, A
15	80	7.1	775	8	US-11-266-748A-133770	Sequence 133770,
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c 17	41.6	3.7	5178	6	US-10-537-017-2	Sequence 2, Appli
18	40.2	3.5	2684	6	US-10-199-229-7	Sequence 7

RESULT 3
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 VERSION U45308.2 GI:6492404
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 SOURCE Synechococcus elongatus PCC 7942
 ORGANISM Synechococcus elongatus PCC 7942
 Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 REFERENCE 1 (bases 1 to 1953)
 AUTHORS Guler,S., Seeliger,A., Hartel,H., Renger,G. and Benning,C.
 TITLE A null mutant of Synechococcus sp. PCC7942 deficient in the sulfolipid sulfoquinovosyl diacylglycerol
 JOURNAL J. Biol. Chem. 271 (13), 7501-7507 (1996)
 PUBMED 8631780
 REFERENCE 2 (bases 1596 to 3104)
 AUTHORS Guler,S., Essigmann,B. and Benning,C.
 TITLE A cyanobacterial gene, sqdX, required for biosynthesis of the sulfolipid sulfoquinovosyldiacylglycerol
 JOURNAL J. Bacteriol. 182 (2), 543-545 (2000)
 PUBMED 10629209
 REFERENCE 3 (bases 1 to 1953)
 AUTHORS Benning,C. and Guler,S.
 TITLE Direct Submission
 JOURNAL Submitted (10-JAN-1996) IGF Berlin, Ihnestr. 63, Berlin 14195, Germany
 REFERENCE 4 (bases 1 to 3104)
 AUTHORS Guler,S., Essigmann,B. and Benning,C.
 TITLE Direct Submission
 JOURNAL Submitted (01-DEC-1999) Dept. of Biochemistry, Michigan State University, East Lansing, MI 10117, USA
 REMARK Sequence update by submitter
 COMMENT On Dec 1, 1999 this sequence version replaced gi:1177752.
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CDS

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ORIGIN

Query Match 100.0%; Score 1134; DB 15; Length 3104;
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 Matches 1134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	181	CCGCTCTATCCCGAGCTGAAGCTAGCTTTTCCGTTGCCGAAAGTGGGAAAAGCCTTGGAG	240
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Db	2100	TACTATGCCAAGGCGCTAAATGTGCCACTCGTGGCGTCCTATCACACCCATTGCGGAAA	2159
Qy	361	TACCTTGAGCATTACGGGCTGGGGGTCTTGGAGGGGGTGCTCTGGGAATTGCTGAAGCTG	420
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Qy	421	GCGCATAACCAAGCAGCGATCAACCTCTGTACTTCAACCGCGATGGTGCAGGAGCTGACA	480
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Qy	721	CTAGAGCAATTGTTTGTCTGGCACCAGACGCAGTTTATTGGCTATCTGCATGGGGAACAG		780
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Qy	781	CTAGGGGCGGCCTACGCTTCTGCTGACGCTTTTGTCTTTCCCTCCCGGACCGAAACCCTC		840
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Qy	901	GGCATTCCCGATATTGTCAGCGACGGCATTAATGGTTTCTGTTTCGATCCTGAGGATGAA		960
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Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
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- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	1134	100.0	1134	6	ABQ75827			Abq75827 Cyanobact
	2	485.6	42.8	1230	13	ADS48039			Ads48039 Bacterial
	3	466.2	41.1	1107	13	ADT45247			Adt45247 Bacterial
	4	161.4	14.2	1633	14	AEB67217			Aeb67217 Rice geno
	5	144.8	12.8	1533	6	ABQ81780			Abq81780 Arabidops
	6	133.4	11.8	1949	13	ADX59805			Adx59805 Plant ful
c	7	126	11.1	615	9	ACL17706			Acl17706 DNA clone
	8	124.4	11.0	1244	13	ADX63809			Adx63809 Plant ful
c	9	120.4	10.6	619	9	ACL17711			Acl17711 DNA clone
	10	119.2	10.5	1344	14	AED46770			Aed46770 Membrane
c	11	117.8	10.4	569	9	ACL17707			Acl17707 DNA clone
	12	117.6	10.4	1221	8	ACA02161			Aca02161 C. glutam

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
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2	96.6	8.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
3	96.6	8.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
4	91.6	8.1	1341	3	US-09-252-991A-12827	Sequence 12827, A
5	64	5.6	1326	3	US-09-328-352-4064	Sequence 4064, Ap
6	63	5.6	714	3	US-09-252-991A-5165	Sequence 5165, Ap
c 7	63	5.6	1251	3	US-09-252-991A-5016	Sequence 5016, Ap
8	63	5.6	1584	3	US-09-252-991A-5109	Sequence 5109, Ap
9	60.8	5.4	1032	3	US-09-902-540-6426	Sequence 6426, Ap
10	60.8	5.4	2632	3	US-09-902-540-440	Sequence 440, App
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Database : EST:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
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c	4	142.6	12.6	961	10	DT518735	DT518735 WS02439.B
	5	141.8	12.5	785	9	DN620750	DN620750 UCRCS11_0
c	6	139.8	12.3	791	10	DV105721	DV105721 chiou0021
	7	139.6	12.3	904	10	DV711665	DV711665 CGN-60518
	8	136.4	12.0	887	8	CO364415	CO364415 RTK1_15_C
	9	136.2	12.0	643	2	BJ258639	BJ258639 BJ258639
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Seq ID NO: 3

Database : GenEmbl:*

- 1: gb_env:*
- 2: gb_pat:*
- 3: gb_ph:*
- 4: gb_pl:*
- 5: gb_pr:*
- 6: gb_ro:*
- 7: gb_sts:*
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- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
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	1	2979	100.0	2979	2	AX615031		AX615031	Sequence
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	3	507.2	17.0	554	8	ATH506242		AJ506242	Arabidops
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c	6	350.6	11.8	1564	4	BT005796		BT005796	Arabidops
c	7	281	9.4	1503	4	AY045961		AY045961	Arabidops
c	8	166	5.6	600	8	ATH506241		AJ506241	Arabidops
c	9	137.2	4.6	134390	4	CT030165		CT030165	M.truncat
c	10	136.6	4.6	1822	4	BT014103		BT014103	Lycopersi
c	11	136.4	4.6	110000	4	AP008207_022		Continuation (23 o	
c	12	136.4	4.6	167405	4	AP002483		AP002483	Oryza sat
c	13	136.4	4.6	175565	4	AP003311		AP003311	Oryza sat
c	14	135.8	4.6	39990	4	AP008222		AP008222	Oryza sat
c	15	135.8	4.6	110000	4	AP008213_000		AP008213	Oryza sat

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
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- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	DB	ID			
	1	2979	100.0	2979	6	ABQ75828			Abq75828 Arabidops
c	2	350.6	11.8	1533	6	ABQ81780			Abq81780 Arabidops
c	3	145	4.9	972	13	ADO81288			Ado81288 Plant ful
c	4	145	4.9	1949	13	ADX59805			Adx59805 Plant ful
c	5	134.2	4.5	651	13	ADX12835			Adx12835 Plant ful
c	6	133.8	4.5	1633	14	AEB67217			Aeb67217 Rice geno
	7	132.4	4.4	569	9	ACL17707			Acl17707 DNA clone
	8	132.4	4.4	615	9	ACL17706			Acl17706 DNA clone

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query				ID	Description
	No.	Score	Match	Length	DB			
c	1	78.4	2.6	174	3	US-09-313-294A-5690		Sequence 5690, Ap
c	2	63	2.1	7218	2	US-08-232-463-14		Sequence 14, Appl
	3	60	2.0	612	3	US-09-902-540-1357		Sequence 1357, Ap
c	4	60	2.0	4403765	3	US-09-103-840A-2		Sequence 2, Appli
c	5	60	2.0	4411529	3	US-09-103-840A-1		Sequence 1, Appli
c	6	59.6	2.0	1141	3	US-09-806-708B-22		Sequence 22, Appl
	7	54.8	1.8	1039	3	US-09-902-540-1280		Sequence 1280, Ap
	8	52	1.7	1141	3	US-09-806-708B-22		Sequence 22, Appl
	9	48.6	1.6	7218	2	US-08-232-463-14		Sequence 14, Appl
c	10	48	1.6	23849	3	US-09-949-016-13813		Sequence 13813, A
c	11	47.4	1.6	1326	3	US-09-328-352-4064		Sequence 4064, Ap
	12	47.4	1.6	2604	3	US-09-839-894-5		Sequence 5, Appli

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Query Match	Length	DB	ID	
	1	416	14.0	866	11	BH468052	BH468052 BOHOJ24TF
	2	383.6	12.9	1279	14	AJ855270	AJ855270 Brassica
c	3	339.6	11.4	1725	6	CNS0A253	BX830044 Arabidops
c	4	324	10.9	806	11	BZ452202	BZ452202 BONO448TR
	5	318.2	10.7	747	11	BH947656	BH947656 obu80c04.
c	6	313.6	10.5	361	11	BH849950	BH849950 SALK_0705
	7	301	10.1	301	11	BH904697	BH904697

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	Query	Match	Length	DB	ID		
No.	Score						
c	1	153.4	5.1	2065	8	US-10-424-599-18773	Sequence 18773, A
c	2	150.4	5.0	2033	8	US-10-424-599-70595	Sequence 70595, A
c	3	145	4.9	972	8	US-10-425-114-8	Sequence 8, Appli
c	4	145	4.9	1949	8	US-10-425-114-30648	Sequence 30648, A
c	5	145	4.9	2077	9	US-10-425-115-47612	Sequence 47612, A
c	6	143.8	4.8	1879	8	US-10-424-599-18772	Sequence

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					ID	Description
	No.	Score	Query Match	Length	DB		
c	1	155	5.2	2093	8	US-11-216-545-1059	Sequence 1059, Ap
c	2	150.4	5.0	1908	8	US-11-216-545-1060	Sequence 1060, Ap
c	3	145	4.9	2850	7	US-11-218-305-18858	Sequence 18858, A
c	4	134.4	4.5	1294	6	US-10-449-902-3517	Sequence 3517, Ap
c	5	134.4	4.5	2131	6	US-10-449-902-15521	Sequence 15521, A
c	6	133.8	4.5	1606	6	US-10-449-902-22084	Sequence 22084, A
c	7	133.8	4.5	1633	6	US-10-449-902-2362	Sequence 2362, Ap
	8	133.8	4.5	1950	7	US-11-218-305-5034	Sequence 5034, Ap
c	9	133.2	4.5	2031	6	US-10-449-902-7919	Sequence 7919, Ap
	10	129.4	4.3	1921	7	US-11-218-305-24481	Sequence 24481, A
	11	126.4	4.2	1314	7	US-11-218-305-24484	Sequence 24484, A
	12	124.8	4.2	1666	7	US-11-218-305-24483	Sequence 24483, A

Seq ID 10: 6

Database : GenEmbl:*

- 1: gb_env:*
- 2: gb_pat:*
- 3: gb_ph:*
- 4: gb_pl:*
- 5: gb_pr:*
- 6: gb_ro:*
- 7: gb_sts:*
- 8: gb_sy:*
- 9: gb_un:*
- 10: gb_vi:*
- 11: gb_ov:*
- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	No.	Score	Query Match Length	DB	ID	
1	1799	100.0	1799	2	AX615033	AX615033 Sequence
2	1799	100.0	1799	2	AX615034	AX615034 Sequence
3	1799	100.0	1799	4	AF022082	AF022082 Arabidops
4	1718	95.5	1797	4	AF380641	AF380641 Arabidops
5	1546.2	85.9	94482	4	ATF26P21	AL031804 Arabidops
6	1546.2	85.9	111876	4	ATF4I10	AL035525 Arabidops
7	1546.2	85.9	198669	4	ATCHRIV78	AL161582 Arabidops
8	1434	79.7	1434	2	CQ805256	CQ805256 Sequence
9	1434	79.7	1434	4	AY113071	AY113071 Arabidops
10	803.8	44.7	1843	4	AY192559	AY192559 Spinacia
11	747.8	41.6	2060	4	AK065310	AK065310 Oryza sat
12	746.2	41.5	2233	4	AK060744	AK060744 Oryza sat
c 13	586.4	32.6	99567	12	AP007324	AP007324 Lotus cor
14	573.4	31.9	111256	4	AC125478	AC125478 Medicago

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1799	100.0	1799	6	ABQ81781	Abq81781 Arabidops
2	1434	79.7	1434	12	ADN73772	Adn73772 Thale cre
3	746.2	41.5	2233	14	AEB67817	Aeb67817 Rice geno
4	519.4	28.9	1143	13	ADT45246	Adt45246 Bacterial
5	505	28.1	1143	13	ADT43979	Adt43979 Bacterial
6	477.4	26.5	1152	13	ADS47906	Ads47906 Bacterial
7	360.6	20.0	572	13	ACN59093	Acn59093 Cotton gy
8	232	12.9	1152	13	ADS61520	Ads61520 Bacterial
9	215.8	12.0	1170	13	ADT43484	Adt43484 Bacterial
10	185.4	10.3	1137	13	ADS58925	Ads58925 Bacterial
11	160	8.9	1212	13	ADS56061	Ads56061 Bacterial
12	144.4	8.0	1182	13	ADT46275	Adt46275 Bacterial
13	143.4	8.0	248	7	ADS66523	Ads66523 Corn seed
14	141.4	7.9	1209	6	ABQ81782	Abq81782

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	46.2	2.6	362	3	US-09-621-976-16509	Sequence 16509, A
2	45	2.5	2915	3	US-09-578-063-72	Sequence 72, Appl
3	45	2.5	2915	5	US-09-333-159-72	Sequence 72, Appl
4	44.4	2.5	2369	3	US-09-057-996-13	Sequence 13, Appl
5	43.4	2.4	1412	3	US-09-614-912-197	Sequence 197, App
6	43	2.4	3338	3	US-09-489-847-117	Sequence 117, App
7	43	2.4	4244	3	US-09-620-312D-151	Sequence 151, App
8	42.6	2.4	1081	3	US-09-372-422A-33	Sequence 33, Appl
c 9	42.4	2.4	611	3	US-09-385-982-70	Sequence 70, Appl
10	42.4	2.4	2830	3	US-09-646-561-25	Sequence 25, Appl

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query				ID	Description
	No.	Score	Match	Length	DB					
	1	1727.2	96.0	1806	6	CNS0A2S1				BX827511 Arabidops
	2	1676.4	93.2	1744	6	CNS0A3AQ				BX826685 Arabidops
	3	1634.2	90.8	1717	6	CNS0A2TO				BX827393 Arabidops
	4	835.2	46.4	953	4	BX836978				BX836978 BX836978
	5	722.8	40.2	803	4	BX836994				BX836994 BX836994
	6	704	39.1	705	7	AV821229				AV821229 AV821229
	7	703.8	39.1	709	4	CB255030				CB255030 52-E01533
	8	696.8	38.7	717	10	DR365949				DR365949 11057256
	9	661	36.7	661	10	DR365956				DR365956 11070500
	10	625.2	34.8	675	9	DR233193				DR233193 12847581
c	11	597	33.2	685	7	AV781569				AV781569

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	833.6	46.3	2017	8	US-10-424-599-32730	Sequence 32730, A
2	719.8	40.0	1910	9	US-10-425-115-46347	Sequence 46347, A
3	519.4	28.9	1143	7	US-10-369-493-43684	Sequence 43684, A
4	505	28.1	1143	7	US-10-369-493-42417	Sequence 42417, A
5	493.2	27.4	1405	8	US-10-437-963-22989	Sequence 22989, A
6	477.4	26.5	1152	7	US-10-369-493-26336	Sequence 26336, A
7	406.6	22.6	1119	8	US-10-767-701-10375	Sequence 10375, A
8	360.6	20.0	572	8	US-10-021-323-13874	Sequence 13874, A
c 9	306	17.0	925	8	US-10-767-701-7240	Sequence 7240, Ap
10	232	12.9	1152	7	US-10-369-493-37194	Sequence 37194, A

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	747.8	41.6	2060	6	US-10-449-902-14764	Sequence 14764, A
2	746.2	41.5	2233	6	US-10-449-902-2962	Sequence 2962, Ap
3	716.6	39.8	1882	7	US-11-218-305-3418	Sequence 3418, Ap
4	529.4	29.4	3248	7	US-11-218-305-3416	Sequence 3416, Ap
5	500.2	27.8	1124	6	US-10-449-902-3777	Sequence 3777, Ap
6	500.2	27.8	1124	6	US-10-449-902-4194	Sequence 4194, Ap
7	46.4	2.6	627	8	US-11-266-748A-52757	Sequence 52757, A
8	46.4	2.6	627	8	US-11-266-748A-209159	Sequence 209159,
9	46	2.6	857	8	US-11-216-545-545	Sequence 545, App
10	45.8	2.5	3720	8	US-11-266-748A-28319	Sequence 28319, A
11	45.2	2.5	1000	8	US-11-266-748A-283925	Sequence 283925,
c 12	45.2	2.5	1000	8	US-11-266-748A-335354	